

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 15, 2003, 14:50:12 ; Search time 18 Seconds  
(without alignments)  
809.904 Million cell updates/sec

Title: US-09-831-805A-6

Perfect score: 1635

Sequence: 1 MALRRPRLRLCARLPDFL.....VNYRTDEGDFRHKSSPVI 310

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	ID	Description
1	483	29.5	JAM2 HUMAN	P57087 homo sapien
2	449.5	27.5	JAM1_MOUSE	O88792 mus musculus
3	419	25.6	JAM1 HUMAN	Q9Y624 homo sapien
4	403.5	24.7	JAM1_BOVIN	Q9Y624 bos taurus
5	231.5	14.2	A33 HUMAN	Q99795 homo sapien
6	186	11.4	NCA1_XENLA	P16170 xenopus lae
7	180	11.0	NCA1_DROME	P15364 drosophila
8	177	10.8	NCA2_XENLA	P36335 xenopus lae
9	171.5	10.5	NCA2_MOUSE	P13594 mus musculus
10	171.5	10.5	NCA1_MOUSE	P13595 mus musculus
11	171	10.5	NEO1_RAT	P97603 rattus norv
12	170.5	10.4	NCA1_RAT	P13596 rattus norv
13	169.5	10.4	PPFD HUMAN	P23468 homo sapien
14	165	10.1	NCM2 HUMAN	O15394 homo sapien
15	164.5	10.1	PKB7_CHICK	Q91048 gallus gall
16	164.5	10.1	PTM7_MOUSE	Q05793 mus musculus
17	164	10.0	NCA2_MOUSE	O35136 mus musculus
18	163.5	10.0	NCA1_BOVIN	P13136 bos taurus
19	163	10.0	NEO1_MOUSE	P97798 mus musculus
20	162.5	9.9	UN89_CAEEL	O01761 caenorhabdi
21	161.5	9.9	CXAR HUMAN	P78310 homo sapien
22	158	9.7	NCA1_CHICK	P13590 gallus gall
23	155.5	9.5	NCA2_HUMAN	P13592 homo sapien
24	155.5	9.5	NCA1_HUMAN	P13591 homo sapien
25	155.5	9.5	NCA1_CHICK	P35331 gallus gall
26	153.5	9.4	NEO1_HUMAN	Q92859 homo sapien
27	153	9.4	NTRI_HUMAN	Q9P121 homo sapien
28	151.5	9.3	LACH_SCHAM	Q26474 schistocerc
29	151	9.2	CEPU_CHICK	Q90773 gallus gall
30	150.5	9.2	CEA5_HUMAN	P06731 homo sapien
31	149.5	9.1	PTPF_HUMAN	P10586 homo sapien
32	149	9.1	LAMP_CHICK	Q98919 gallus gall
33	148.5	9.1	LAMP_RAT	Q62813 rattus norv

## RESULT 1

JAM2_HUMAN	148.5	9.1	646	1	MU18_HUMAN	P43121	homo sapien
ID	AC	P57087	STANDARD	PRT	298 AA	Q99pJ0	mus musculus
DT	16-OCT-2001	(Rel. 40, Created)				Q62718	rattus norv
DT	16-OCT-2001	(Rel. 40, Last sequence update)				Q13449	homo sapien
DE	15-SEP-2003	(Rel. 42, Last annotation update)				P97792	mus musculus
DE	Junctional adhesion molecule 2 precursor (Vascular endothelial					P32736	rattus norv
DE	junction-associated molecule) (VE-JAM)					P98160	homo sapien
GN	JAM2 OR VEJAM OR C21ORP43					P31809	mus musculus
OS	Homo sapiens (Human)					Q90610	gallus gall
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					P11834	bos taurus
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					P22063	rattus norv
OX	NCBI_TaxID=9606;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RC	TISSUE=Vascular endothelial cells;						
EX	MEDLINE=20317114; PubMed=10779521;						
RA	Palmeri D., van Zante A., Huang C.C., Hemmerich S., Rosen S.D.;						
RT	"Vascular endothelial junction-associated molecule, a novel member of						
RT	the immunoglobulin superfamily, is localized to intercellular						
RT	boundaries of endothelial cells."						
RL	J. Biol. Chem. 275:19139-19145(2000).						
RN	[2]						
RP	SEQUENCE FROM N.A.						
RC	TISSUE=Placenta;						
EX	MEDLINE=20507930; PubMed=10945976;						
RA	Cunningham S.A., Arrate M.P., Rodriguez J.M., Bjerkce R.J.,						
RA	Vanderslice P., Morris A.P., Brock T.A.;						
RT	"A novel protein with homology to the junctional adhesion molecule:						
RT	Characterization of leukocyte interactions."						
RL	J. Biol. Chem. 275:34750-34756(2000).						
RN	[3]						
RP	SEQUENCE FROM N.A.						
RC	TISSUE=Lung;						
EX	MEDLINE=2388257; PubMed=12477932;						
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,						
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,						
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,						
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,						
RA	Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,						
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,						
RA	Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,						
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,						
RA	Bozak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,						
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,						
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,						
RA	Faney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,						
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,						
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,						
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,						
RA	Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,						
RA	Schneerch A., Schein J.E., Jones S.J.M., Marra M.A.;						
RT	"Generation and initial analysis of more than 15,000 full-length						
RT	human and mouse cDNA sequences."						
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).						

## ALIGNMENTS



```
DR MGD: MGI:1321398; Flr1.  
DR InterPro: IPR007110; Ig-like.  
DR InterPro: IPR003006; Ig MHC.  
DR InterPro: IPR003596; Ig_v.  
DR Pfam: PF00047; Ig; 2.  
DR SMART: SM00406; IgV; 1.  
DR PROSITE: PS00835; IG LIKE; 2.  
KW Tight junction; Immunoglobulin domain; Glycoprotein; Transmembrane;  
KW Repeat; Signal; 3D-structure.  
FT SIGNAL 1 26  
FT CHAIN 27 300 JUNCTIONAL ADHESION MOLECULE 1.  
FT DOMAIN 27 338 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 239 259 POTENTIAL.  
FT DOMAIN 260 299 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 28 122 IG-LIKE V-TYPE 1.  
FT DOMAIN 134 230 IG-LIKE V-TYPE 2.  
FT DISULFID 49 108 POTENTIAL.  
FT DISULFID 152 212 POTENTIAL.  
FT CARBOHYD 42 42 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 185 185 N-LINKED (GLCNAC. .) (POTENTIAL).  
SQ SEQUENCE 300 AA; 32368 MW; 391F3E48FE3B97EC CRC64;  
  
Query Match 27.5%; Score 449.5; DB 1; Length 300;  
Best Local Similarity 35.2%; Pred. No. 1.1e-30;  
Matches 105; Conservative 56; Mismatches 122; Indels 15; Gaps 7;  
  
Qy 20 LLLPRGCLIGAV-----NLKSSNRPVVPQFESVELSCLITDSQTSPPRIEWKKIQDEQ 74  
Db 11 LLFLETSMLGSLVGKGSVYTAQDVQVPENESIKLTC--TYSGFSSPRVWEKVFQGST 68  
Qy 75 TTYVPFDNKIQGLAGRAEILGKTSKLWNVTRDSALYRCVEAVNRDKIDEIVIELT 134  
Db 69 TALVCYNSQITAPYADRV-TPSSSGITFSSVTRKNGEYTC-WVSEEGQYNGEVSIIHT 126  
Qy 135 VQVKVPTVCPVKAPVKGKATLHCQSEGHPRPHYSWYRNDVPLPT-DSRANRPRFNS 193  
Db 127 VLVPPSKPTISVPSSVITGNRAVLTCSEHDGSPSEYSNFKDGISMLTADAKTKRAFNS 186  
Qy 194 SSSLNSETGLVFTAVHKDDSQYICIASNDAGSA-RCEQBMVEYVDNLNIGIIGVLVW 252  
Db 187 SFTIDPKSGDLIFDPTAFDSEYVQQAQNGVGTAMRSEAHMADVNLNIGIIVAVLVT 246  
Qy 253 LAVLALITLIGCCAYRRGYFINNKQDGSYKPNKPGDGVNVRTDEGDFRHKSSFVI 310  
Db 247 LILLGLLIFGVWFAYSRGVFETTKG----TAPGKKVIYSQPSISEGEFKTSSEFLV 300  
  
RESULT 3  
ID JAM1 HUMAN STANDARD; PRT; 299 AA.  
AC Q9Y6Z4;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Junctional adhesion molecule 1 precursor (JAM) (Platelet adhesion  
DE molecule 1) (PAM-1) (Platelet F11 receptor).  
GN F11R OR JAM1 OR JCAM.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99323940; PubMed=10395639;  
RA Ozaki H., Ishii K., Horiuchi H., Arai H., Kawamoto T., Okawa K.,  
RA Iwamatsu A., Kita T.;  
RT "Combined treatment of TNF-alpha and IFN-gamma causes redistribution  
RT of junctional adhesion molecule in human endothelial cells.";  
RL J. Immunol. 163:553-557(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Sobocka M.B., Sobocki T., Rushbrook J.I., Banerjee P., Weiss C.,  
RA Kornecki E.;
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RT "Molecular cloning and sequencing of the cDNA of F11 receptor, a  
RT novel Ig superfamily member from human platelets";  
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Naik U.P., Naik M.U., DeLeon P., Szychala J.;  
RA "Cloning and characterization of PAM-1, a novel platelet adhesion  
RT molecule involved in platelet activation";  
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=21154917; PubMed=11230166;  
RA Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,  
RA Ansong W., Blocher M., Bloecker H., Bauersachs S., Blum H.,  
RA Lauber J., Dueterhoeft A., Beyer A., Koehler K., Strack N.,  
RA Mewes H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D.,  
RA Wambutt R., Korn B., Klein M., Poustka A.;  
RA "Towards a catalog of human genes and proteins: sequencing and  
RT analysis of 500 novel complete protein coding human cDNAs";  
RL Genome Res. 11:422-435(2001).  
CC -!- FUNCTION: Seems to play a role in epithelial tight junction  
CC formation. Appears early in primordial forms of cell junctions and  
CC recruits PARD3. The association of the PARD6-PARD3 complex may  
CC prevent the interaction of PARD3 with JAM1, thereby preventing  
CC tight junction assembly (By similarity). Plays a role in  
CC regulating monocyte transmigration involved in integrity of  
CC epithelial barrier. Involved in platelet activation.  
CC -!- SUBUNIT: Interacts with the first PDZ domain of PARD3. The  
CC association between PARD3 and PARD6B probably disrupts this  
CC interaction (By similarity).  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
CC -!- TISSUE SPECIFICITY: Localized at tight junctions of both  
CC epithelial and endothelial cells.  
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.  
CC -!- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC use by non-profit institutions as long as its content is in no way  
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CC entities requires a license agreement. See http://www.ebi.ac.uk/announcements  
CC or send an email to license@ebi.ac.uk.  
CC -----  
CC EMBL: AF111713; AAD42050.1; -  
CC EMBL: AF207907; AAF22829.1; -  
CC EMBL: AF172398; AAD48877.1; -  
CC EMBL: AL136649; CAB66584.1; -  
CC PIR: A59406; S56749.  
CC Genew: HGNC:14685; F11R.  
CC MIM: 605721; -  
CC GO: GO:0006954; P:inflammatory response; TAS.  
CC InterPro: IPR007110; Ig-like.  
CC InterPro: IPR003006; Ig MHC.  
CC InterPro: IPR003596; Ig_v.  
CC Pfam: PF00047; Ig; 2.  
CC SMART: SM00406; IgV; 1.  
CC PROSITE: PS00835; IG LIKE; 2.  
KW Tight junction; Immunoglobulin domain; Glycoprotein; Transmembrane;  
KW Repeat; Signal.  
FT SIGNAL 1 25 POTENTIAL.  
FT CHAIN 26 299 EXTRACELLULAR (POTENTIAL).  
FT DOMAIN 26 238 POTENTIAL.  
FT TRANSMEM 239 259 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 260 299 IG-LIKE V-TYPE 1.  
FT DOMAIN 27 125 IG-LIKE V-TYPE 2.  
FT DOMAIN 135 228 POTENTIAL.  
FT DISULFID 50 109 POTENTIAL.  
FT DISULFID 153 212 POTENTIAL.  
FT CARBOHYD 185 185 N-LINKED (GLCNAC. .) (POTENTIAL).  
SQ SEQUENCE 299 AA; 32583 MW; D95DE2FEA23D2851 CRC64;
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Query Match      25.6%; Score 419; DB 1; Length 299;
Best Local Similarity 32.8%; Pred. No. 4e-28;
Matches 101; Conservative 47; Mismatches 138; Indels 22; Gaps 7;

QY 8 RRLICARLPDFFLLFRGCLIGAVNLKSSNRTFVQEFESVELSCIITDSQSDPREW 67
DB 9 RKLLCL----FILAILLCLSLGSLVTHSSSEFEVRIPEPNPVKLSLAY--SGFSSPRV 62
QY 68 KKIQDEQTYVFFDNKIQDLAGRAEILGKTSLKWNVTRDSALYRCVVARNDKREID 127
DB 63 KPDQDTRLCVNNKIIITASVEDRTFEL-PTGITKSVTRDGTGYTC-MVSEEGNSYG 120
QY 128 EIVIELTVQVKEVTPVCRVPKAVPVGMATLHCQSEGHPRPHYSWYRNDVPLPTDSRAN 187
DB 121 EVKKVLIIVLPSPKPTNIPSSATIGNRAVLTCSEQDQSPPEYTWPKDGIWPTNPST 180
QY 188 PRFNSSSHLSETGLTFTAVHKDDSGQYCYCIASNDAGSARCEBQ-EMEYVDNLIGGII 246
DB 181 RAFNSSSYVLNPTTGGELVDFPLSDTGEYSCEARNGYGTPTMTSNAVRMEAVERNVIV 240
QY 247 GGVLVLAVALITLIGICAVRRGYFINNKODGES----YKNPKPGDGVNVRTDDEGDF 302
DB 241 AAVLVTLILLGLVFGIWFAYSRGHFDRTKGTSSKKVIYSQPS-----ARSEGEF 291
QY 303 RHKSSFVI 310
DB 292 KQTSSFLV 299

RESULT 4
JAM1_BOVIN
ID JAM1_BOVIN STANDARD; PRT; 298 AA.
AC Q9XT56.
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Junctional adhesion molecule 1 precursor (JAM).
GN F1R OR JAM1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99223940; PubMed=10395639;
RA Ozaki H., Ishii K., Horiuchi H., Arai H., Kawamoto T., Okawa K.,
RA Iwamatsu A., Kita T.;
RT "Combined treatment of TNF-alpha and IFN-gamma causes redistribution
RL of junctional adhesion molecule in human endothelial cells.";
RL J. Immunol. 163:553-557(1999).
CC -!- FUNCTION: Seems to play a role in epithelial tight junction
CC formation. Appears early in primordial forms of cell junctions and
CC recruits PAR3. The association of the PAR6-PARD3 complex may
CC prevent the interaction of PAR3 with JAM1, thereby preventing
CC tight junction assembly (By similarity). Plays a role in
CC regulating monocyte transmigration involved in integrity of
CC epithelial barrier. Involved in platelet activation.
CC -!- SUBUNIT: Interacts with the first PDZ domain of PAR3. The
CC association between PAR3 and PAR6B probably disrupts this
CC interaction (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -!- TISSUE SPECIFICITY: Localized at tight junctions of both
CC epithelial and endothelial cells.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN V-TYPE DOMAINS.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC EMBL; AF111714; AAD2051.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_C2.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00408; IGG2; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
KW Tight junction; Immunoglobulin domain; Glycoprotein; Transmembrane;
KW Repeat; Signal.
FT SIGNAL 1 24
FT CHAIN 25 298
FT DOMAIN 25 237
FT TRANSMEM 238 258
FT DOMAIN 259 298
FT DOMAIN 28 124
FT DOMAIN 134 227
FT DISULFID 49 108
FT DISULFID 152 211
FT CARBOHYD 184 184
SQ SEQUENCE 298 AA; 32456 MW; 714FE1C1714769A2 CRC64;

Query Match      24.7%; Score 403.5; DB 1; Length 298;
Best Local Similarity 33.8%; Pred. No. 8.2e-27;
Matches 102; Conservative 48; Mismatches 125; Indels 27; Gaps 10;

QY 21 LLFRGGLI-----GAVNLKSSNRTPVQ--EFESVELSCIITDSQSDPREWKKIQ 71
DB 12 LLFTSMILCSLALGRGAV----QTYEPVVRVPPNNPAKLSG--SYSGFSPRVWEKETH 65
QY 72 DEQTYVFFDNKIQDLAGRAEILGKTSLKWNVTRDSALYRCVVARNDKREIDIVI 131
DB 66 GDIRGLVCYNNKITASYENRV-TFSDTGITHSVTRKDTGMYTC-MVSEGGNTYGEVTV 123
QY 132 ELTVQVKEVTPVCRVPKAVPVGMATLHCQSEGHPRPHYSWYRNDVPLPTDSRANPFR 191
DB 124 QLIVLPSPKPTINVPSSVTIGTRAVLTCSEKSDGSPSEYKWKFDGVEMPLEKSNRAPS 183
QY 192 NSSSHLSENGTGLTFTAVHKDDSGQYCYCIASND-AGSARCEBQEMEVYVDNLIGGIVL 250
DB 184 NSSVTLLQKTELIFDPVPSASDTGDTGTCQONGVSPVKSVDTVHMDAVELNVGGIVAAVF 243
QY 251 VVLAVLALITLIGICAVRRGYFINNKODGESYKPKPGDGVNVRTD--EEGDFRHKSSF 308
DB 244 VTLILLGLALIFGIWFAYSRGIFDRAKK-GTSNKK-----VIYQPNARSDEGFEQTSSF 296
QY 309 VI 310
DB 297 LV 298

RESULT 5
A33_HUMAN
ID A33_HUMAN STANDARD; PRT; 319 AA.
AC Q99795;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Cell surface A33 antigen precursor (Glycoprotein A33).
GN GPA33.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Colon carcinoma;
RX MEDLINE=97165045; PubMed=9012807;
RA Heath J.K., White S.J., Johnstone C.N., Catimel B., Simpson R.J.,
RA Moritz R.L., Tu G.-F., Ji H., Whitehead R.H., Groenen L.C.,
RA Scott A.M., Ritter G., Cohen L., Welt S., Old L.J., Nice E.C.,
RA Burgess A.W.;
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DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00047; ig; 5.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00408; IGC2; 5.
DR PROSITE; PS00835; IG-LIKE; 5.
KW Cell adhesion; Glycoprotein; Transmembrane; Repeat; Brain;
KW Immunoglobulin domain; Alternative splicing; Signal.
FT SIGNAL 1 19
FT CHAIN 20 1088
FT FT
FT FT
FT DOMAIN 20 705
FT TRANSMEM 706 723
FT DOMAIN 724 1088
FT DOMAIN 724 1088
FT DOMAIN 20 108
FT DOMAIN 113 202
FT DOMAIN 209 294
FT DOMAIN 303 397
FT DOMAIN 400 484
FT DOMAIN 512 589
FT DOMAIN 618 686
FT DOMAIN 149 153
FT DOMAIN 158 162
FT DISULFID 41 93
FT DISULFID 136 186
FT DISULFID 232 282
FT DISULFID 323 379
FT DISULFID 420 473
FT CARBOHYD 82 82
FT CARBOHYD 219 219
FT CARBOHYD 310 310
FT CARBOHYD 341 341
FT CARBOHYD 417 417
FT CARBOHYD 443 443
FT CARBOHYD 472 472
FT VARSPIC 804 1049
FT SQ
SQ SEQUENCE 1088 AA; 117778 MW; 62738B55B03F3B83 CRC64;

Query Match 11.4%; Score 186; DB 1; Length 1088;
Best Local Similarity 29.9%; Pred. No. 98-08; 82; Indels 36; Gaps 12;
Matches 63; Conservative 30; Mismatches 92;

QY 30 GAVNLK-----SSNRTPVQPEFSELSCTIIDSQDPF-IEWK-KIQDEQTTVFFDN 82
Db 105 GTVNLKIYKLTFFKNAPTQPEFKEGEDAVIICDVSSIPSITWRHKGK-----VIFKK 159
QY 83 KIQGLAGRAEILGKTSKIMNVRDRSALYRCE--VVARND--RKEIDEIV-IELTVQV 137
Db 160 DV-----RFVVLANNYLQIRGKTKDEGTYRCEGRILARGEINKYDIQVINVPPTIQA 213
QY 138 KPTVPVCRVPKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSHL 197
Db 214 RQL-----RVNATANMAESVVLSC-DADGFPDPPEISWLKKGEP-EDGEKISF----- 260
QY 198 NSETGLVFTAVHKDDSGGYCIANSNAGSA 228
Db 261 NEDQSEMTIHVVEKDDAEYSIANNQAGEA 291

RESULT 7
AMAL DROME
ID AMAL DROME STANDARD; PRT; 333 AA.
AC P15364; O9V3A5;
DT 01-APR-1990 (Rel. 14, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Amalgam protein precursor.
GN AMA OR-BG:DS00276.6 OR CG2198.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;

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RN RP SEQUENCE FROM N.A.
RC STRAIN=Oregon-R;
RX MEDLINE=89028670; PubMed=3141062;
RA Seger M.A., Haffley L., Kaufman T.C.;
RT "Characterization of amalgam: a member of the immunoglobulin
RL superfamily from Drosophila.";
RL Cell 55:589-600 (1989).
RN RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RA Celniker S.E., Pfeiffer B.D., Knafels J., Martin C.H., Mayeda C.A.,
RA Palazzolo M.J.;
RT "Complete sequence of the Antennapedia complex of Drosophila.";
RT Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazef R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Fertiera S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glaeser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei Y., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195 (2000).
RN RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley; TISSUE=Embryo;
RX MEDLINE=22426066; PubMed=12537569;
RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
RA George R.A., Guarin H., Kronmiller B., Pacle J.M., Park S., Wan K.H.,
RA Rubin G.M., Celniker S.E.;
RT "A Drosophila full-length cDNA resource.";
RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8 (2002).
CC -!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
CC (POSSIBLE).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
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CC -----  
 CC EMBL; M23561; AAA28367.1; -  
 DR EMBL; AE001572; AAD19797.1; -  
 DR EMBL; AE003674; AAF54084.1; -  
 DR EMBL; AY051911; AAK93335.1; -  
 DR PIR; A31923; A31923.  
 DR FlyBase; FBgn0000071; Ama.  
 DR GO; GO:0005886; C:plasma membrane; IDA.  
 DR InterPro; IPR007110; IG\_Like.  
 DR InterPro; IPR003598; IG\_C2.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR Pfam; PF00047; IG; 3  
 DR SMART; SM00408; IGC2; 2.  
 DR PROSITE; PS50835; IG\_Like; 3.  
 KW Immunoglobulin domain; Glycoprotein; GPI-anchor; Signal; Repeat.  
 FT SIGNAL 1 23  
 FT CHAIN 24 ?  
 FT PROPEP ? 333  
 FT DOMAIN 25 128  
 FT DOMAIN 139 223  
 FT DOMAIN 230 323  
 FT DISULFID 46 117  
 FT DISULFID 161 208  
 FT DISULFID 251 307  
 FT CARBOHYD 45 45  
 FT CARBOHYD 86 86  
 FT CARBOHYD 308 308  
 FT CONFLICT 83 83  
 FT CONFLICT Q -> K (IN REF. 1).  
 SQ SEQUENCE 333 AA; 36387 MW; F644753DE3DB25F1 CRC64;

Query Match 11.0%; Score 180; DB 1; Length 333;

Best Local Similarity 26.8%; Pred. No. 6.6e-08;  
 Matches 52; Conservative 39; Mismatches 83; Indels 20; Gaps 5;

OY 35 KSSNTPVQVFESVELSCIIITSDSPRIEMKKIQDEQTYVFDNKIQDLAGRAEI 94  
 DB 143 ENTPTKTLTVEQNLELIC--HANGFPKPTISWAR-----EHNAMVAGGHL 187  
 OY 95 LKTSKIKWNVTRDSALYRCVWVARNDKKEIDEIVIELTVQVKPTVPCRVKAPVVGK 154  
 DB 188 LAEPLRLRSVHRMDRGYYC--IAQNGEGQDKELIRVEFRQIAVQRPKIAQMWSH 245  
 OY 155 MATLHCQSEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSHLNSETGLVFTAVHKDD 214  
 DB 246 SAELEC-SVOGYPAPTVVMHKNVGL--QSSRHEVANTASSSGTTTSLVRIDSVGEEDF 302  
 OY 215 GQYCIASNDAGSA 228  
 DB 303 GDYCNATNKGHA 316

#### RESULT 8

ID\_NCA2\_XENLA STANDARD; PRT; 1092 AA.  
 AC P36335;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Neural cell adhesion molecule 2, 180 kDa isoform precursor (N-CAM  
 DE 180).  
 GN NCAM2.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8335;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RX MEDLINE=93273239; PubMed=7684721;  
 RA Tonissen K.F., Krieg P.A.;  
 RT "Two neural-cell adhesion molecule (NCAM)-encoding genes in Xenopus  
 RL laevis are expressed during development and in adult tissues.";  
 RL Gene 127:243-247(1993)  
 CC -!- FUNCTION: THIS PROTEIN IS A CELL ADHESION MOLECULE INVOLVED IN  
 CC NEURON-NEURON ADHESION, NEURITE FASCICULATION, OUTGROWTH OF  
 CC NEURITES, ETC.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event-Alternative splicing; Named isoforms=1;  
 CC Comment=A number of isoforms are produced;  
 CC Name=1;  
 CC IsoId=P36335-1; Sequence=Displayed;  
 CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.  
 CC -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.  
 CC -!- SIMILARITY: Contains 2 fibronectin type III domains.  
 CC -----  
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CC -----  
 CC EMBL; M76710; AAA49910.1; -  
 DR PIR; JN0635; JN0635.  
 DR HSP; P56276; 1TLK.  
 DR InterPro; IPR003961; FN III.  
 DR InterPro; IPR007110; IG-Like.  
 DR InterPro; IPR003598; IG\_C2.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR Pfam; PF00041; fn3; 2.  
 DR Pfam; PF00047; fn3; 5.  
 DR SMART; SM00060; FN3; 2.  
 DR SMART; SM00408; IGC2; 4.  
 DR PROSITE; PS50835; IG\_Like; 5.  
 KW Cell adhesion; Glycoprotein; Transmembrane; Repeat; Brain;  
 KW Immunoglobulin domain; Alternative splicing; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 1092  
 FT DOMAIN 20 705  
 FT TRANSMEM 706 723  
 FT DOMAIN 724 1092  
 FT DOMAIN 20 108  
 FT DOMAIN 113 202  
 FT DOMAIN 208 295  
 FT DOMAIN 303 397  
 FT DOMAIN 400 489  
 FT DOMAIN 512 589  
 FT DOMAIN 618 686  
 FT DOMAIN 149 153  
 FT DOMAIN 158 162  
 FT DISULFID 41 93  
 FT DISULFID 136 186  
 FT DISULFID 232 282  
 FT DISULFID 323 379  
 FT DISULFID 420 473  
 FT CARBOHYD 82 82  
 FT CARBOHYD 219 219  
 FT CARBOHYD 310 310  
 FT CARBOHYD 341 341  
 FT CARBOHYD 417 417  
 FT CARBOHYD 443 443  
 FT CARBOHYD 472 472  
 SQ SEQUENCE 1092 AA; 118082 MW; CD236E0EF8B7AD1 CRC64;

Query Match 10.8%; Score 177; DB 1; Length 1092;  
 Best Local Similarity 29.5%; Pred. No. 5.2e-07;  
 Matches 62; Conservative 28; Mismatches 86; Indels 34; Gaps 11;

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Qy 30 GAVNLKSSNR-----TPVQVFESVELSCIITDSQSDPR-IEWK-KIQDQTTVVFDDN 82
Dy 105 GTVNLKIYQKLTFFKYPPTQFTEGEDAVIICDVSSSIPSIITWRHKGKD-----VIFPK 159
Qy 83 KIQDLAGRAEILGKTSKINVTFRDSDALYRCE--VVARNDKREIDIVIELTVQVQKPV 140
Dy 160 DV-----RFVVLANNYLQIRGIKTKTSGNYRCEGRILARG---EINYKDIQVIVNPPL 210
Qy 141 TPV--CRYPKAVPVCKMATLKQESGEHPRHYSWYRNDVPLPTDSRANPRFRSSSHLN 198
Dy 211 IQARQIRVNANMDESIVLSC-DADGPDPEISWLKKGEPIT-EDGEBKISF-----N 261
Qy 199 SETGLVFTAVHKDPSGOYCIASNDAGSA 228
Dy 262 EDKSEMTYRVEKEDAEAYSICIANNOAGEA 291

RESULT 9
ID_NCA2 MOUSE STANDARD; PRT; 725 AA.
AC P13594; Q61950;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Neural cell adhesion molecule 1, 120 kDa isoform precursor (N-CAM 120)
DE (NCAM-120).
GN NCAM1 OR NCAM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=87246524; PubMed=3595563;
RA Barths D., Santoni M.-J., Wille M., Ruppert C., Caix J.-C.,
RA Hirsch M.-R., Fontecilla-Camps J.-C., Goridis C.;
RT "Isolation and nucleotide sequence of mouse NCAM cDNA that codes for
RL a Mr 79,000 polypeptide without a membrane-spanning region.";
RN [2]
RP SEQUENCE OF 20-700 FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=89251563; PubMed=2721486;
RA Santoni M.-J., Barths D., Vopper G., Boned A., Goridis C., Wille M.;
RT "Differential exon usage involving an unusual splicing mechanism
RL generates at least eight types of NCAM cDNA in mouse brain.";
RN [3]
RP SEQUENCE OF 642-725 FROM N.A.
RX MEDLINE=88283628; PubMed=3396534;
RA Barbas J.A., Chaix J.-C., Steinmetz M., Goridis C.;
RT "Differential splicing and alternative polyadenylation generates
RL distinct NCAM transcripts and proteins in the mouse.";
RN [4]
RP SEQUENCE OF 20-36.
RX MEDLINE=86140120; PubMed=3512556;
RA Rougon G., Marshak D.R.;
RT "Structural and immunological characterization of the amino-terminal
RL domain of mammalian neural cell adhesion molecules.";
RN [5]
RP J. Biol. Chem. 261:3396-3401(1986).
CC -!- FUNCTION: THIS PROTEIN IS A CELL ADHESION MOLECULE INVOLVED IN
CC NEURON-NEURON ADHESION, NEURITE FASCICULATION, OUTGROWTH OF
CC NEURITES, ETC.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=N-CAM 120;
CC IsoId=P13594-1; Sequence=Displayed;
CC Name=N-CAM 180;
CC IsoId=P13595-1; Sequence=External;
CC Name=N-CAM 140;

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CC CC IsoId=P13595-2; Sequence=External;
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 2 fibronectin type III domains.
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CC or send an email to license@isb-sib.ch).
CC CC EMBL; Y00051; CAA68263.1; -
CC EMBL; X15049; CAA33148.1; ALT_SEQ.
CC EMBL; X07195; CAA30173.1; -
CC PIR; A29673; IJMSNG.
CC PDB; 2NCM; 12-MAR-97.
CC PDB; 3NCM; 23-JUL-99.
CC MGD; MGI:97281; Ncam1.
CC InterPro; IPR003961; FN III.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003598; Ig_C2.
CC InterPro; IPR003006; Ig_MHC.
CC Pfam; PF00041; fn3; 2.
CC Pfam; PF00047; Ig; 5.
CC SMART; SM00060; FN3; 2.
CC SMART; SM00408; IGC2; 5.
CC PROSITE; PS00835; IG_LIKE; 5.
CC Cell adhesion; Glycoprotein; Repeat; Alternative splicing;
CC Immunoglobulin domain; Signal; Heparin-binding; GPI-anchor;
CC 3D-structure.
CC SIGNAL 1 19
CC CHAIN 20 725
CC FT DOMAIN 20 111
CC FT DOMAIN 116 205
CC FT DOMAIN 212 302
CC FT DOMAIN 309 402
CC FT DOMAIN 407 492
CC FT DOMAIN 519 596
CC FT DOMAIN 152 625
CC FT DOMAIN 161 165
CC FT DISULFID 41 96
CC FT DISULFID 139 189
CC FT DISULFID 235 288
CC FT DISULFID 330 386
CC FT DISULFID 427 480
CC FT CARBOHYD 222 222
CC FT CARBOHYD 316 316
CC FT CARBOHYD 348 348
CC FT CARBOHYD 424 424
CC FT CARBOHYD 450 450
CC FT CARBOHYD 479 479
CC FT CONFLICT 261 268
CC FT CONFLICT 273 273
CC FT CONFLICT 354 355
CC FT CONFLICT 549 549
CC FT CONFLICT 572 572
CC FT CONFLICT 575 575
CC FT CONFLICT 589 594
CC FT CONFLICT 600 602
CC FT CONFLICT 657 657
CC SEQUENCE 725 AA; 80296 MW; C2AE8B84461C6B2F CRC64;
CC Query Match 10.5%; Score 171.5; DB 1; Length 725;
CC Best Local Similarity 27.3%; Pred. No. 9.1e-07;
CC Matches 63; Conservative 41; Mismatches 84; Indels 43; Gaps 12;
Qy 27 CLIGA-----VNLKSSNR-----TPVQVFESVELSCIITDSQSDPR-IEWK 71
Dy 96 CVVTAEDGTQSEATVNVKIFQKLMFNAPTQEFKEGSDAVIVCDVSSLPPTIWK--- 152

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FT CARBOHYD 479 479 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 810 1076 Missing (in isoform N-CAM 140).
FT FTIG=VSP 002588.
SQ SEQUENCE 1115 AA; 119351 MW; 2C93D0D474CFBCAF CRC64;

Query Match 10.5%; Score 171.5; DB 1; Length 1115;
Best Local Similarity 27.3%; Pred. No. 1.6e-06;
Matches 63; Conservative 41; Mismatches 84; Indels 43; Gaps 12;

QY 27 CLIGA-----VNLKSSNR-----TPVQEPESVLSLCTITDSQTS-DPIRWKKIQ 71
DQ 96 CVVTAEDGTQSEATVNVKIFQKMPKNAFTPOEFKEGEDAVIVCDVSSLSPTTIWK--- 152
QY 72 DEQTTVFFDKIQGLAGRAILGKTSIKIWNVTRRDSALYRCB--VVARNDKKEIDEI 129
DQ 153 -----HKGRDVLKKDV--RFIVLSNVLYQIRGIKKTDEGTVRCGRILARG---EINFK 202
QY 130 VIELTVQKVPVTPVCR--VPKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPLPTDSRAN 187
DQ 203 DIQVNVVPEPTVQARQSVNATANLQSVTLVC-DADGFPEPTMTSKDGEPIENEER-D 260
QY 188 PFRNSSSHLNSCTGLVFTAVHKDDSGYVCIASNDAGSARCEOEVEVY 238
DQ 261 ERSRSV-----SDSEVTIRNVDRKDEAEYVCIENKAG-----EQDASIH 302

RESULT 11
NEOL_RAT
ID NEOL_RAT STANDARD; PRT; 1377 AA.
AC P97603;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Neogenin precursor (Fragment).
GN NEOL OR NGN.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1] SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97015074; PubMed=8861902;
RA Keino-Masu K., Masu M., Hink L., Leonardo E.D., Chan S.S.-Y.,
RA Culotti J.G., Tessier-Lavigne M.;
RA "Deleted in Colorectal Cancer (DCC) encodes a netrin receptor.";
RL Cell 87:175-185(1996).
CC -!- FUNCTION: MAY BE INVOLVED AS A REGULATORY PROTEIN IN THE
CC TRANSITION OF UNDIFFERENTIATED PROLIFERATING CELLS TO THEIR
CC DIFFERENTIATED STATE. MAY ALSO FUNCTION AS A CELL ADHESION
CC MOLECULE IN A BROAD SPECTRUM OF EMBRYONIC AND ADULT TISSUES.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. DCC
CC SUBFAMILY.
CC -!- SIMILARITY: Contains 4 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 6 fibronectin type III domains.
CC
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CC -----
CC EMBL; U68726; AAB41100.1; -.
CC HSSP; P56276; 1TLK.
CC InterPro; IPR003961; FN III.
CC InterPro; IPR003962; FNIII subd.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003598; Ig_C2.
CC InterPro; IPR003006; Ig_MHC.
CC Pfam; PF00041; fn3; 6.

DR PFam; PF00047; ig; 4.
DR PRINTS; PR00014; FNTYPEIII.
DR SMART; SM00060; FN3; 6.
DR SMART; SM00408; IGC2; 3.
DR PROSITE; PS00835; IG-LIKE; 4.
KW Cell adhesion; Repeat; Signal; Transmembrane; Immunoglobulin domain;
KW Glycoprotein.
FT NON TER 1 1
FT CHAIN <1 2
FT SIGNAL 3 1377
FT CHAIN 3 1074
FT DOMAIN 3 1074
FT TRANSMEM 1075 1095
FT DOMAIN 1096 1377
FT DOMAIN 21 114
FT DOMAIN 121 206
FT DOMAIN 198 305
FT DOMAIN 310 395
FT DOMAIN 405 502
FT DOMAIN 505 598
FT DOMAIN 599 698
FT DOMAIN 704 798
FT DOMAIN 819 919
FT DOMAIN 920 1021
FT DOMAIN 1087 1090
FT DISULFID 43 98
FT DISULFID 142 190
FT DISULFID 239 289
FT DISULFID 331 379
FT CARBOHYD 42 42
FT CARBOHYD 179 179
FT CARBOHYD 295 295
FT CARBOHYD 439 439
FT CARBOHYD 458 458
FT CARBOHYD 608 608
FT CARBOHYD 684 684
FT CARBOHYD 878 878
SQ SEQUENCE 1377 AA; 150637 MW; E514ED8AD1A63A9 CRC64;

Query Match 10.5%; Score 171; DB 1; Length 1377;
Best Local Similarity 31.0%; Pred. No. 2.2e-06;
Matches 61; Conservative 21; Mismatches 69; Indels 46; Gaps 9;

QY 47 EVELSCITITDSQTSQSDPRIWKIODEQTTVFFDKIQGLAGRAELIGTSLKWNVT 106
DQ 233 QSAVLPVCA--SGLPAPVIRWKNEDVLT-----ESSGRLLALLAGSLEISDV 280
QY 107 RDSALTRCEVVARNDKKEIDEIVIELTVQKVPVPCVRKAVPVGKMATLHCQES--- 163
DQ 281 EDDAGTYPC--VADNGNKTI-EAQALTVQVPPF-----LKQANIYARESM 327
QY 164 -----EGHPRPHYSWYRN-DVPLPTDSRANPRFRNSSSHLNSCTGLVFTAVHKDDSGQ 216
DQ 328 VFCEVTGKPAPTVMKNGDVVIPS-----YFKIVKEH-----NLQVLGLVKSDEGF 376
QY 217 YCIASNDAGSARCEEQ 233
DQ 377 YQCIENDVGNQAQAQ 393

RESULT 12
NEOL_RAT
ID NEOL_RAT STANDARD; PRT; 858 AA.
AC P13596;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Neural cell adhesion molecule 1, 140 kDa isoform precursor (N-CAM 140)
DE (NCAM-140).
GN NCAM1 OR NCAM.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
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FN SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RA MEDLINE=88059265; PubMed=3680385;  
RX Small S.J., Shull G.E., Santoni M.-J., Akesson R.;  
RT "Identification of a cDNA clone that contains the complete coding  
sequence for a 140-kD rat NCAM polypeptide."  
RL J. Cell Biol. 105:2335-2345(1987).  
RN [2]  
RP SEQUENCE OF 355-364 FROM N.A.  
RX MEDLINE=90166485; PubMed=2483053;  
RA Small S.J., Haines S.L., Akesson R.A.;  
RT "Polypeptide variation in an N-CAM extracellular immunoglobulin-like  
fold is developmentally regulated through alternative splicing."  
RL Neuron 1:1007-1017(1988).  
CC -!- FUNCTION: THIS PROTEIN IS A CELL ADHESION MOLECULE INVOLVED IN  
CC NEURON-NEURON ADHESION, NEURITE FASCICULATION, OUTGROWTH OF  
CC NEURITES, ETC.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=1;  
CC Comment=A number of isoforms are produced;  
CC Name=1;  
CC IsoId=P13596-1; Sequence=Displayed;  
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.  
CC -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.  
CC -!- SIMILARITY: Contains 2 fibronectin type III domains.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; X06564; CAA29809.1; -;  
DR EMBL; M32611; AAA41679.1; -;  
DR PIR; S00846; IJRTNC.  
DR PDB; 1EPF; 27-OCT-00.  
DR InterPro; IPR003961; FN\_III.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003598; IG\_c2.  
DR InterPro; IPR003006; IG\_MHC.  
DR Pfam; PF00041; fn3; 2.  
DR Pfam; PF00047; ig; 5.  
DR SMART; SM00060; FN3; 2.  
DR SMART; SM00408; IGC2; 5.  
DR PROSITE; PS50835; IG LIKE; 5.  
KW Cell adhesion; Glycoprotein; Transmembrane; Repeat;  
KW Immunoglobulin domain; Alternative splicing; Signal; Heparin-binding;  
KW 3D-structure.  
FT SIGNAL 1 19  
FT CHAIN 20 858  
FT  
FT DOMAIN 20 721  
FT TRANSMEM 722 739  
FT POTENTIAL.  
FT CYTOPLASMIC (POTENTIAL).  
FT IG-LIKE C2-TYPE 1.  
FT IG-LIKE C2-TYPE 2.  
FT IG-LIKE C2-TYPE 3.  
FT IG-LIKE C2-TYPE 4.  
FT IG-LIKE C2-TYPE 5.  
FT FIBRONECTIN TYPE-III 1.  
FT FIBRONECTIN TYPE-III 2.  
FT HEPARIN-BINDING (POTENTIAL).  
FT HEPARIN-BINDING (POTENTIAL).  
FT BY SIMILARITY.  
FT BY SIMILARITY.  
FT BY SIMILARITY.  
FT BY SIMILARITY.  
FT BY SIMILARITY.  
FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT

FT CARBOHYD 316 316 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 348 348 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 434 434 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 460 460 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 489 489 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 858 AA; 94658 MW; EAIAUG6AEAO5S0F6 CRC64;  
Query Match 10.4%; Score 170.5; DB 1; Length 858;  
Best Local Similarity 26.3%; Pred. No. 1.4e-06;  
Matches 61; Conservative 41; Mismatches 85; Indels 45; Gaps 12;  
QY 27 CLIGA-----VNLKSSNR-----TPVQVESVLSCLITDSQTS-DPIEWKKIQ 71  
DB 96 CVVTAEDGTQSEATVNVKIFQKLMFKNAPTQPEKGEADVIVCDVWSLPTIWK--- 152  
QY 72 DEQTYVFFDKIOGDLAERAEILKTSKLNWVTRRDSALYRCE--VVARNDKKEIDEI 129  
DB 153 -----HKGRDVILKRDV--RFVLSNNYLQIRGKKTDEGYRCEGRILARG---EINFK 202  
QY 130 VIETVQVKPTVPVCR--VPRKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPLPTDSRAN 187  
DB 203 DIQIVNVVPTVQARQISVNAVATANIGQSVTLVC-DADGFPEPTMSWTKDGEPIENE--- 258  
QY 188 PRFRNSSSHL-NSETGLVFTAVHKDSDGQYVCIASNDAGSARCEEQEMEYV 238  
DB 259 ---EDDEKHIFSDSDSELTIKRVNDKDEAEYVCAENKAG-----EQDASIH 302  
RESULT 13  
PTPD HUMAN  
ID PTPD HUMAN STANDARD; PRT; 1912 AA.  
AC P23468;  
DT 01-NOV-1991 (Rel. 20, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Protein-tyrosine phosphatase delta precursor (EC 3.1.3.48) (R-PTP-  
DE delta).  
GN PTPRD.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF ARG-1178.  
RX MEDLINE=95204468; PubMed=7896816;  
RA Pulido R., Krueger N.X., Serra-Pages C., Saito H., Streuli M.;  
RT "Molecular characterization of the human transmembrane protein-  
RT tyrosine phosphatase delta. Evidence for tissue-specific expression of  
RT alternative human transmembrane protein-tyrosine phosphatase delta  
RT isoforms.";  
RL J. Biol. Chem. 270:6722-6728(1995).  
RN [2]  
RP SEQUENCE OF 390-1912 FROM N.A.  
RC TISSUE=Placenta;  
RX MEDLINE=91006018; PubMed=2170109;  
RA Krueger N.X., Streuli M., Saito H.;  
RT "Structural diversity and evolution of human receptor-like protein  
RT tyrosine phosphatases.";  
RL EMBO J. 9:3241-3252(1990).  
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein  
CC tyrosine + phosphate.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=3;  
CC Comment=Additional isoforms seem to exist;  
CC Name=1;  
CC IsoId=P23468-1; Sequence=Displayed;  
CC Name=2; Synonyms=Kidney;  
CC IsoId=P23468-2; Sequence=VSP\_005147, VSP\_005148, VSP\_005149;  
CC Name=3; Synonyms=Fetal brain;  
CC IsoId=P23468-3; Sequence=VSP\_005150;  
CC -!- PTM: A CLEAVAGE OCCURS THAT SEPARATES THE EXTRACELLULAR DOMAIN  
CC FROM THE TRANSMEMBRANE SEGMENT.



```
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00047; ig; 5.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00408; IGC2; 5.
DR PROSITE; PS50835; IG LIKE; 5.
KW Cell adhesion; Transmembrane; Glycoprotein; Repeat;
KW Immunoglobulin domain; Signal.
FT SIGNAL 1 19
FT CHAIN 20 837
FT DOMAIN 20 697
FT TRANSMEM 698 718
FT DOMAIN 719 837
FT DOMAIN 21 108
FT DOMAIN 113 202
FT DOMAIN 208 297
FT DOMAIN 302 396
FT DOMAIN 401 491
FT DOMAIN 482 581
FT DOMAIN 594 678
FT DISULFID 42 93
FT DISULFID 136 186
FT DISULFID 232 282
FT DISULFID 322 380
FT DISULFID 422 475
FT CARBOHYD 177 177
FT CARBOHYD 219 219
FT CARBOHYD 309 309
FT CARBOHYD 406 406
FT CARBOHYD 419 419
FT CARBOHYD 445 445
FT CARBOHYD 474 474
FT CARBOHYD 562 562
SQ SEQUENCE 837 AA; 52932 MW; C3D034106C5741C1 CRC64;

Query Match 10.1%; Score 165; DB 1; Length 837;
Best Local Similarity 24.3%; Pred. No. 3.9e-06;
Matches 72; Conservative 31; Mismatches 105; Indels 88; Gaps 15;

QY 44 QEF---ESVELSCITDQSDPRLEWKIKQDEQTYVFFNKIOGDLAAGRAEILGKTSL 100
Db 124 QEFKQGEDAEVVCVRVSSPA--PAVSWLYHNEVTT--ISDN-----RLAMLANNL 171
QY 101 KINWTRDSALYRCE--VVARNDKREIDEIVIELTVQKPTVPCVRPKAVPV----- 152
Db 172 QILNINKSDEGIYRCGEVRKE-----IDFRDIIVVNPVPPAISMWPKQSFN 219
QY 153 -----GKMATLHCQSEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSHLNSETGLTVFT 207
Db 220 ATAERGEEMTSCRAS-GSPEPAISWFRNGKLE-----ENEKYLKGSNTELTVR 269
QY 208 AVHKDDSGQYCIANDGASRCQEVEVDNLNGIIGVVLVLAVALITIGICAY 267
Db 270 NIINSDGGPVCRATNKAG-----EDEKQAF-----LQVFQVPHIQLKNETTY 313
QY 268 RRGYFINNKQGESYKNPKP-----DGVNYIRTEGDPR-----HKSS 307
Db 314 ENQGVTLVCDAB-----GEPIPEITWKRAVDGFTTEGDKSPDGRIEVKGQHGSS 363

RESULT 15
PTK7 CHICK
ID PTK7 CHICK STANDARD; PRT; 1051 AA.
AC Q91048;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tyrosine-protein kinase-like 7 precursor (Kinase like protein).
GN PTK7 OR KLG.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

NCBI\_TaxID=9031;

11

SEQUENCE FROM N.A.

TISSUE=Embryonic brain;

MEDLINE=91271300; PubMed=1711213;

Chou Y.-H., Hayman M.J.;

"Characterization of a member of the immunoglobulin gene superfamily that possibly represents an additional class of growth factor receptor";

Proc. Natl. Acad. Sci. U.S.A. 88:4897-4901(1991).

-!- FUNCTION: MAY FUNCTION AS A CELL ADHESION MOLECULE. LACKS PROBABLY THE CATALYTIC ACTIVITY OF TYROSINE KINASE.

-!- SUBCELLULAR LOCATION: Type I membrane protein.

-!- TISSUE SPECIFICITY: EXPRESSED IN BONE MARROW, SPLEEN, BURSA, THYMUS AND BRAIN. WEAKLY EXPRESSED IN FIBROBLASTS. ALSO EXPRESSED IN EMBRYONIC LIVER.

-!- SIMILARITY: Contains 7 immunoglobulin-like C2-type domains.

-!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. INSULIN RECEPTOR SUBFAMILY.

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EMBL; M63437; AAA48933.1; -.

PIR; A39712; A39712.

HSSP; P12931; 1FWK.

InterPro; IPR007110; Ig-like.

InterPro; IPR003598; Ig\_c2.

InterPro; IPR003006; Ig\_MHC.

InterPro; IPR001245; Tyr\_kinase.

Pfam; PF00047; ig; 7.

Pfam; PF00069; pkinase; 1.

PRINTS; PR00109; TYRKINASE.

ProDom; PD000001; Prot\_kinase; 1.

SMART; SM00408; IGC2; 4.

SMART; SM00219; TyrKc; 1.

PROSITE; PS50835; IG LIKE; 7.

PROSITE; PS50011; PROTEIN KINASE DOM; 1.

PROSITE; PS00109; PROTEIN KINASE TYR; 1.

Receptor; Transmembrane; Signal; Glycoprotein; Cell adhesion; Immunoglobulin domain; Repeat.

SIGNAL 1 22

CHAIN 23 1051

DOMAIN 23 685

TRANSMEM 686 706

DOMAIN 707 1051

DOMAIN 23 105

DOMAIN 115 204

DOMAIN 213 298

DOMAIN 308 388

DOMAIN 393 472

DOMAIN 487 566

DOMAIN 573 661

DOMAIN 777 1048

DISULFID 40 88

DISULFID 137 187

DISULFID 234 282

DISULFID 326 372

DISULFID 414 462

DISULFID 505 551

DISULFID 594 645

CARBOHYD 103 103

CARBOHYD 202 202

CARBOHYD 255 255

CARBOHYD 264 264

POTENTIAL.

TYROSINE-PROTEIN KINASE-LIKE 7.

EXTRACELLULAR (POTENTIAL).

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

IG-LIKE C2-TYPE 1.

IG-LIKE C2-TYPE 2.

IG-LIKE C2-TYPE 3.

IG-LIKE C2-TYPE 4.

IG-LIKE C2-TYPE 5.

IG-LIKE C2-TYPE 6.

IG-LIKE C2-TYPE 7.

PROTEIN KINASE; INACTIVE.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 444 444 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 548 548 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 627 627 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 1051 AA; 116366 MW; 175242AEAA4CB702 CRC64;

Query Match 10.1%; Score 164.5; DB 1; Length 1051;  
Best Local Similarity 24.5%; Pred. No. 5.6e-06;  
Matches 66; Conservative 35; Mismatches 109; Indels 59; Gaps 11;

QY 40 TPVVQEFESVE-----LSCIITDSQSDPRIEWKKIQDEQTYVFFDNKIQGDLGRAE 93  
DB 486 PPPPQLOCFMEFNEKVTVSCSATGRE--KPTIQWTKTD-----GSSLPSHVSHRAG 534  
QY 94 ILGKTSLKIMNVTRRDSALYRCEVVARNDRKEIDEIVIELTVQVKPVTVCVRPKAVPVG 153  
DB 535 I-----LSFHKVSRSDSGNYTC--IASNSPQGEIRATVQLVVAVVVTFKLEPEPTTVYQG 587  
QY 154 KMATLHCOESEGHPHYSWYRNDVPLPTDGRANFRNSSHLSNSETGLVFTAVHKDD 213  
DB 588 HTAMFQCQ-AEGDPVPHIQWKGDKIL-DPSKLLPRIQIMPN-----GSLVIVDVTTED 639  
QY 214 SGQYYCIASNDAG-----SARCEQF-----MEVVDLNIIGGIIGVIV 251  
DB 640 SGKYTCTIAGNSCNIKHREAFLYVVDKPAAEDEGSPSHTPYKMIQTIGLSVGAAYAYIII 699  
QY 252 VLAVLALITLGICCAVRRGYFINNKQDGE 280  
DB 700 VLGLMF-----YCKKRRKAKRLKKHPEGE 723

Search completed: December 15, 2003, 14:52:33  
Job time : 20 secs